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(54) Title: METHOD OF TREATING TNF-DEPENDENT INFLAMMATION USING TUMOR NECROSIS FACTOR ANTAGONISTS (57) Abstract A method for treating TNF-dependent inflammatory diseases in a mammal by administering a TNF antagonist, such as soluble TNFR.		

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TITLE

Method of Treating TNF-Dependent Inflammation Using Tumor Necrosis Factor Antagonists

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CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of U.S. application Serial No. 523,635, filed May 10, 1990, now pending, which is a continuation-in-part of U.S. application Serial No. 421,417, filed October 13, 1989, now abandoned, which is a
10 continuation-in-part of U.S. application Serial No. 405,370, filed September 11, 1989, now abandoned, which is a continuation-in-part of U.S. application Serial No. 403,241, filed September 5, 1989, now abandoned.

BACKGROUND OF THE INVENTION

15 The present invention relates generally to cytokine receptors and more specifically to a method of using tumor necrosis factor antagonists to suppress TNF-dependent inflammatory diseases.

Tumor necrosis factor- α (TNF α , also known as cachectin) and tumor necrosis factor- β (TNF β , also known as lymphotoxin) are homologous mammalian endogenous
20 secretory proteins capable of inducing a wide variety of effects on a large number of cell types. The great similarities in the structural and functional characteristics of these two cytokines have resulted in their collective description as "TNF." Complementary cDNA clones encoding TNF α (Pennica et al., *Nature* 312:724, 1984) and TNF β (Gray et al., *Nature* 312:721, 1984) have been isolated, permitting further structural and
25 biological characterization of TNF.

TNF proteins initiate their biological effect on cells by binding to specific TNF receptor (TNFR) proteins expressed on the plasma membrane of a TNF-responsive cell. Two distinct forms of TNFR are known to exist: Type I TNFR (TNFR I), having a molecular weight of approximately 75 kilodaltons, and Type II TNFR (TNFR II),
30 having a molecular weight of approximately 55 kilodaltons. TNFR I and TNFR II each bind to both TNF α and TNF β . TNFR I and TNFR II have both been molecularly cloned (Smith et al., *Science* 248:1019, 1990; Loetscher et al., *Cell* 61:351, 1990 and Schall et al., *Cell* 61:361, 1990), permitting recombinant expression and purification of soluble TNFR proteins.

35 Soluble TNF binding proteins from human urine have also been identified (Peetre et al., *Eur. J. Haematol.* 41:414, 1988; Seckinger et al., *J. Exp. Med.* 167:1511, 1988; Seckinger et al., *J. Biol. Chem.* 264:11966, 1989; UK Patent

Application, Publ. No. 2 218 101 A to Seckinger et al.; Engelmann et al., *J. Biol. Chem.* 264:11974, 1989).

5 TNF antagonists, such as soluble TNFR and TNF binding proteins, bind to TNF and prevent TNF from binding to cell membrane bound TNF receptors. Such proteins may therefore be useful to suppress biological activities caused by TNF.

10 The role of TNF in mediated inflammatory diseases and the *in vivo* biological effects of such soluble TNFR and TNF binding protein proteins in suppressing such TNF-dependent inflammatory diseases have not been fully elucidated and potential therapeutic uses for TNF antagonists have yet to be identified.

SUMMARY OF THE INVENTION

15 The present invention provides a method of using TNF antagonists to suppress TNF-dependent inflammatory diseases. Specifically, the present invention provides a method of treating a human having arthritis comprising the step of administering a TNF antagonist, such as soluble human TNFR, to a human.

These and other aspects of the present invention will become evident upon reference to the following detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

20 FIGURE 1 shows the dimeric structure of the recombinant human TNFR/Fc fusion protein. The primary translation product of the plasmid coding for rhu TNFR/Fc is a single molecule of soluble TNFR linked to single chain of Fc derived from human IgG1. Following translation, but prior to secretion, this fusion molecule dimerizes via 3 cysteine residues in the Fc region to form dimeric rhu TNFR/Fc.

25 Boxes denote structural domains of TNFR.

FIGURE 2 shows the construction of plasmid pCAVDHFR rhu TNFR/Fc. Abbreviations are as follows: ADH2, yeast alcohol dehydrogenase gene and regulatory region; CMV, cytomegalovirus immediate early enhancer; TPL, adenovirus-2 tripartite leader; VA, adenovirus-2 virus-associated RNA genes I and II; DHFR, hamster dihydrofolate reductase gene.

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FIGURES 3 and 4 are graphs showing the effect of intra-articular administration of recombinant human TNFR/Fc, monomeric TNFR, recombinant murine IL-1R and TNFR monomer combined with rmuIL-1R on antigen-induced arthritis in rats. The data indicate that TNFR/Fc, TNFR monomer, rmu IL-1R and

35 TNFR combined with IL-1R suppress inflammation associated with antigen-induced arthritis.

FIGURE 5 shows the effect of intraperitoneal administration of recombinant human TNFR/Fc and PBS (vehicle control) on the development of collagen induced arthritis (CIA) in B10.RIII mice. TNFR/Fc significantly delayed the onset of CIA.

FIGURE 6 shows the effect of intraperitoneal administration of recombinant human TNFR/Fc and PBS (vehicle control) on the development of collagen induced arthritis (CIA) in DBA/1 mice. TNFR/Fc significantly delayed the onset of CIA.

FIGURE 7 shows that administration of TNFR/Fc in mice reduced the arthritis index and the number of joints showing signs of arthritis.

10 DETAILED DESCRIPTION OF THE INVENTION

Definitions

As used herein, the terms "TNF receptor" and "TNFR" refer to proteins having amino acid sequences which are substantially similar to the native mammalian TNF receptor or TNF binding protein amino acid sequences, and which are capable of binding TNF molecules and inhibiting TNF from binding to cell membrane bound TNFR. Two distinct types of TNFR are known to exist: Type I TNFR (TNFRI) and Type II TNFR (TNFRII). The mature full-length human TNFRI is a glycoprotein having a molecular weight of about 75-80 kilodaltons (kDa). The mature full-length human TNFRII is a glycoprotein having a molecular weight of about 55-60 kilodaltons (kDa). The preferred TNFRs of the present invention are soluble forms of TNFRI and TNFRII, as well as soluble TNF binding proteins. Soluble TNFR molecules include, for example, analogs or subunits of native proteins having at least 20 amino acids and which exhibit at least some biological activity in common with TNFRI, TNFRII or TNF binding proteins. Soluble TNFR constructs are devoid of a transmembrane region (and are secreted from the cell) but retain the ability to bind TNF. Various bioequivalent protein and amino acid analogs have an amino acid sequence corresponding to all or part of the extracellular region of a native TNFR, for example, huTNFRIΔ235, huTNFRIΔ185 and huTNFRIΔ163, or amino acid sequences substantially similar to the sequences of amino acids 1-163, amino acids 1-185, or amino acids 1-235 of SEQ ID NO:1, and which are biologically active in that they bind to TNF ligand. Equivalent soluble TNFRs include polypeptides which vary from these sequences by one or more substitutions, deletions, or additions, and which retain the ability to bind TNF or inhibit TNF signal transduction activity via cell surface bound TNF receptor proteins, for example huTNFRIΔx, wherein x is selected from the group consisting of any one of amino acids 163-235 of SEQ ID NO:1. Analogous deletions may be made to muTNFR. Inhibition of TNF signal transduction activity can be determined by transfecting cells with recombinant TNFR DNAs to obtain recombinant receptor expression. The cells are then contacted with TNF and the resulting metabolic

effects examined. If an effect results which is attributable to the action of the ligand, then the recombinant receptor has signal transduction activity. Exemplary procedures for determining whether a polypeptide has signal transduction activity are disclosed by Idzerda et al., *J. Exp. Med.* 171:861 (1990); Curtis et al., *Proc. Natl. Acad. Sci. USA* 86:3045 (1989); Prywes et al., *EMBO J.* 5:2179 (1986) and Chou et al., *J. Biol. Chem.* 262:1842 (1987). Alternatively, primary cells or cell lines which express an endogenous TNF receptor and have a detectable biological response to TNF could also be utilized.

The nomenclature for TNFR analogs as used herein follows the convention of naming the protein (e.g., TNFR) preceded by either hu (for human) or mu (for murine) and followed by a Δ (to designate a deletion) and the number of the C-terminal amino acid. For example, huTNFR Δ 235 refers to human TNFR having Asp²³⁵ as the C-terminal amino acid (i.e., a polypeptide having the sequence of amino acids 1-235 of SEQ ID NO:1). In the absence of any human or murine species designation, TNFR refers generically to mammalian TNFR. Similarly, in the absence of any specific designation for deletion mutants, the term TNFR means all forms of TNFR, including mutants and analogs which possess TNFR biological activity.

The term "isolated" or "purified", as used in the context of this specification to define the purity of TNFR protein or protein compositions, means that the protein or protein composition is substantially free of other proteins of natural or endogenous origin and contains less than about 1% by mass of protein contaminants residual of production processes. Such compositions, however, can contain other proteins added as stabilizers, carriers, excipients or co-therapeutics. TNFR is isolated if it is detectable as a single protein band in a polyacrylamide gel by silver staining.

"Recombinant," as used herein, means that a protein is derived from recombinant (e.g., microbial or mammalian) expression systems. "Microbial" refers to recombinant proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a protein produced in a microbial expression system which is essentially free of native endogenous substances. Protein expressed in most bacterial cultures, e.g., *E. coli*, will be free of glycan. Protein expressed in yeast may have a glycosylation pattern different from that expressed in mammalian cells.

"Biologically active," as used throughout the specification as a characteristic of TNF receptors, means that a particular molecule shares sufficient amino acid sequence similarity with the embodiments of the present invention disclosed herein to be capable of binding detectable quantities of TNF, transmitting a TNF stimulus to a cell, for example, as a component of a hybrid receptor construct, or cross-reacting with anti-TNFR antibodies raised against TNFR from natural (i.e., nonrecombinant) sources. Preferably, biologically active TNF receptors within the scope of the present invention

are capable of binding greater than 0.1 nmoles TNF per nmole receptor, and most preferably, greater than 0.5 nmole TNF per nmole receptor in standard binding assays (see below).

5 Soluble TNF Antagonists and Analogs

The present invention utilizes isolated and purified TNF antagonist polypeptides. The isolated and purified TNF antagonist polypeptides used in this invention are substantially free of other contaminating materials of natural or endogenous origin and contain less than about 1% by mass of protein contaminants residual of production processes. The TNF antagonist polypeptides used in this
10 invention are optionally without associated native-pattern glycosylation.

In preferred aspects of the present invention, the TNF antagonists are selected from the group consisting of soluble human TNFRI and TNFRII. The pCAV/NOT-TNFR vector, containing the human TNFRI cDNA clone 1, was used to express and
15 purify soluble human TNFRI. pCAV/NOT-TNFR has been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD 20852, USA (Accession No. 68088) under the name pCAV/NOT-TNFR.

Like most mammalian genes, mammalian TNF receptors are presumably encoded by multi-exon genes. Alternative mRNA constructs which can be attributed to
20 different mRNA splicing events following transcription, and which share large regions of identity or similarity with the cDNAs claimed herein may also be used.

Other mammalian TNFR cDNAs may be isolated by using an appropriate human TNFR DNA sequence as a probe for screening a particular mammalian cDNA library by cross-species hybridization. Mammalian TNFR used in the present invention
25 includes, by way of example, primate, human, murine, canine, feline, bovine, ovine, equine and porcine TNFR. Mammalian TNFRs can be obtained by cross species hybridization, using a single stranded cDNA derived from the human TNFR DNA sequence as a hybridization probe to isolate TNFR cDNAs from mammalian cDNA libraries.

Derivatives of TNFR which may be used in the present invention also include
30 various structural forms of the primary protein which retain biological activity. Due to the presence of ionizable amino and carboxyl groups, for example, a TNFR protein may be in the form of acidic or basic salts, or may be in neutral form. Individual amino acid residues may also be modified by oxidation or reduction.

The primary amino acid structure may be modified by forming covalent or
35 aggregative conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like, or by creating amino acid sequence mutants. Covalent derivatives are prepared by linking particular functional groups to TNFR

amino acid side chains or at the N- or C-termini. Other derivatives of TNFR include covalent or aggregative conjugates of TNFR or its fragments with other proteins or polypeptides, such as by synthesis in recombinant culture as N-terminal or C-terminal fusions. For example, the conjugated peptide may be a signal (or leader) polypeptide sequence at the N-terminal region of the protein which co-translationally or post-translationally directs transfer of the protein from its site of synthesis to its site of function inside or outside of the cell membrane or wall (e.g., the yeast α -factor leader). TNFR protein fusions can comprise peptides added to facilitate purification or identification of TNFR (e.g., poly-His). The amino acid sequence of TNF receptor can also be linked to the peptide Asp-Tyr-Lys-Asp-Asp-Asp-Lys (DYKDDDDK) (Hopp et al., *Bio/Technology* 6:1204,1988.) The latter sequence is highly antigenic and provides an epitope reversibly bound by a specific monoclonal antibody, enabling rapid assay and facile purification of expressed recombinant protein. This sequence is also specifically cleaved by bovine mucosal enterokinase at the residue immediately following the Asp-Lys pairing. Fusion proteins capped with this peptide may also be resistant to intracellular degradation in *E. coli*.

TNFR with or without associated native-pattern glycosylation may also be used. TNFR expressed in yeast or mammalian expression systems, e.g., COS-7 cells, may be similar or slightly different in molecular weight and glycosylation pattern than the native molecules, depending upon the expression system. Expression of TNFR DNAs in bacteria such as *E. coli* provides non-glycosylated molecules. Functional mutant analogs of mammalian TNFR having inactivated N-glycosylation sites can be produced by oligonucleotide synthesis and ligation or by site-specific mutagenesis techniques. These analog proteins can be produced in a homogeneous, reduced-carbohydrate form in good yield using yeast expression systems. N-glycosylation sites in eukaryotic proteins are characterized by the amino acid triplet Asn-A₁-Z, where A₁ is any amino acid except Pro, and Z is Ser or Thr. In this sequence, Asn provides a side chain amino group for covalent attachment of carbohydrate. Such a site can be eliminated by substituting another amino acid for Asn or for residue Z, deleting Asn or Z, or inserting a non-Z amino acid between A₁ and Z, or an amino acid other than Asn between Asn and A₁.

TNFR derivatives may also be obtained by mutations of TNFR or its subunits. A TNFR mutant, as referred to herein, is a polypeptide homologous to TNFR but which has an amino acid sequence different from native TNFR because of a deletion, insertion or substitution.

Bioequivalent analogs of TNFR proteins may be constructed by, for example, making various substitutions of residues or sequences or deleting terminal or internal residues or sequences not needed for biological activity. For example, cysteine

residues can be deleted (e.g., Cys¹⁷⁸) or replaced with other amino acids to prevent formation of unnecessary or incorrect intramolecular disulfide bridges upon renaturation. Other approaches to mutagenesis involve modification of adjacent dibasic amino acid residues to enhance expression in yeast systems in which KEX2 protease activity is present. Generally, substitutions should be made conservatively; i.e., the most preferred substitute amino acids are those having physiochemical characteristics resembling those of the residue to be replaced. Similarly, when a deletion or insertion strategy is adopted, the potential effect of the deletion or insertion on biological activity should be considered. Substantially similar polypeptide sequences, as defined above, generally comprise a like number of amino acids sequences, although C-terminal truncations for the purpose of constructing soluble TNFRs will contain fewer amino acid sequences. In order to preserve the biological activity of TNFRs, deletions and substitutions will preferably result in homologous or conservatively substituted sequences, meaning that a given residue is replaced by a biologically similar residue. Examples of conservative substitutions include substitution of one aliphatic residue for another, such as Ile, Val, Leu, or Ala for one another, or substitutions of one polar residue for another, such as between Lys and Arg; Glu and Asp; or Gln and Asn. Other such conservative substitutions, for example, substitutions of entire regions having similar hydrophobicity characteristics, are well known. Moreover, particular amino acid differences between human, murine and other mammalian TNFRs is suggestive of additional conservative substitutions that may be made without altering the essential biological characteristics of TNFR.

Subunits of TNFR may be constructed by deleting terminal or internal residues or sequences. Particularly preferred sequences include those in which the transmembrane region and intracellular domain of TNFR are deleted or substituted with hydrophilic residues to facilitate secretion of the receptor into the cell culture medium. The resulting protein is referred to as a soluble TNFR molecule which retains its ability to bind TNF. A particularly preferred soluble TNFR construct is TNFRIΔ235 (the sequence of amino acids 1-235 of SEQ ID NO:1), which comprises the entire extracellular region of TNFRI, terminating with Asp²³⁵ immediately adjacent the transmembrane region. Additional amino acids may be deleted from the transmembrane region while retaining TNF binding activity. For example, huTNFRIΔ183 which comprises the sequence of amino acids 1-183 of SEQ ID NO:1, and TNFRIΔ163 which comprises the sequence of amino acids 1-163 of SEQ ID NO:1, retain the ability to bind TNF ligand. TNFRIΔ142, however, does not retain the ability to bind TNF ligand. This suggests that one or both of Cys¹⁵⁷ and Cys¹⁶³ is required for formation of an intramolecular disulfide bridge for the proper folding of TNFRI. Cys¹⁷⁸, which was deleted without any apparent adverse effect on the ability of the soluble TNFRI to

bind TNF, does not appear to be essential for proper folding of TNFRI. Thus, any deletion C-terminal to Cys¹⁶³ would be expected to result in a biologically active soluble TNFRI. The present invention contemplates use of such soluble TNFR constructs corresponding to all or part of the extracellular region of TNFR terminating
5 with any amino acid after Cys¹⁶³. Other C-terminal deletions, such as TNFRIA157, may be made as a matter of convenience by cutting TNFR cDNA with appropriate restriction enzymes and, if necessary, reconstructing specific sequences with synthetic oligonucleotide linkers. Soluble TNFR with N-terminal deletions may also be used in the present invention. For example, the N-terminus of TNFRI may begin with Leu¹,
10 Pro² or Ala³ without significantly affecting the ability of TNFRI to effectively act as a TNF antagonist. The resulting soluble TNFR constructs are then inserted and expressed in appropriate expression vectors and assayed for the ability to bind TNF.

Mutations in nucleotide sequences constructed for expression of analog TNFR must, of course, preserve the reading frame phase of the coding sequences and
15 preferably will not create complementary regions that could hybridize to produce secondary mRNA structures such as loops or hairpins which would adversely affect translation of the receptor mRNA. Although a mutation site may be predetermined, it is not necessary that the nature of the mutation *per se* be predetermined. For example, in order to select for optimum characteristics of mutants at a given site, random
20 mutagenesis may be conducted at the target codon and the expressed TNFR mutants screened for the desired activity.

Not all mutations in the nucleotide sequence which encodes TNFR will be expressed in the final product, for example, nucleotide substitutions may be made to enhance expression, primarily to avoid secondary structure loops in the transcribed
25 mRNA (see EPA 75,444A, incorporated herein by reference), or to provide codons that are more readily translated by the selected host, e.g., the well-known *E. coli* preference codons for *E. coli* expression.

Mutations can be introduced at particular loci by synthesizing oligonucleotides containing a mutant sequence, flanked by restriction sites enabling ligation to fragments
30 of the native sequence. Following ligation, the resulting reconstructed sequence encodes an analog having the desired amino acid insertion, substitution, or deletion.

Alternatively, oligonucleotide-directed site-specific mutagenesis procedures can be employed to provide an altered gene having particular codons altered according to the substitution, deletion, or insertion required. Exemplary methods of making the
35 alterations set forth above are disclosed by Walder et al. (*Gene* 42:133, 1986); Bauer et al. (*Gene* 37:73, 1985); Craik (*BioTechniques*, January 1985, 12-19); Smith et al. (*Genetic Engineering: Principles and Methods*, Plenum Press, 1981); and U.S. Patent

Nos. 4,518,584 and 4,737,462 disclose suitable techniques, and are incorporated by reference herein.

Both monovalent forms and polyvalent forms of TNFR may also be used in the present invention. Polyvalent forms possess multiple TNFR binding sites for TNF ligand. For example, a bivalent soluble TNFR may consist of two tandem repeats of amino acids 1-235 of SEQ ID NO:1, separated by a linker region. Alternate polyvalent forms may also be constructed, for example, by chemically coupling TNFR to any clinically acceptable carrier molecule, a polymer selected from the group consisting of Ficoll, polyethylene glycol or dextran using conventional coupling techniques. Alternatively, TNFR may be chemically coupled to biotin, and the biotin-TNFR conjugate then allowed to bind to avidin, resulting in tetravalent avidin/biotin/TNFR molecules. TNFR may also be covalently coupled to dinitrophenol (DNP) or trinitrophenol (TNP) and the resulting conjugate precipitated with anti-DNP or anti-TNP-IgM, to form decameric conjugates with a valency of 10 for TNFR binding sites.

A recombinant chimeric antibody molecule may also be produced having TNFR sequences substituted for the variable domains of either or both of the immunoglobulin molecule heavy and light chains and having unmodified constant region domains. For example, chimeric TNFR/IgG₁ may be produced from two chimeric genes -- a TNFR/human κ light chain chimera (TNFR/C κ) and a TNFR/human γ_1 heavy chain chimera (TNFR/C γ_1). Following transcription and translation of the two chimeric genes, the gene products assemble into a single chimeric antibody molecule having TNFR displayed bivalently. Such polyvalent forms of TNFR may have enhanced binding affinity for TNF ligand. One specific example of a TNFR/Fc fusion protein is disclosed in SEQ ID NO:3 and SEQ ID NO:4. Additional details relating to the construction of such chimeric antibody molecules are disclosed in WO 89/09622 and EP 315062.

Expression of Recombinant TNFR

Recombinant expression vectors are preferably used to amplify or express DNA encoding TNFR to obtain purified TNFR. Recombinant expression vectors are replicable DNA constructs which have synthetic or cDNA-derived DNA fragments encoding mammalian TNFR or bioequivalent analogs operably linked to suitable transcriptional or translational regulatory elements derived from mammalian, microbial, viral or insect genes. A transcriptional unit generally comprises an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, transcriptional promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription and translation initiation and termination sequences, as described in detail below. Such

regulatory elements may include an operator sequence to control transcription, a sequence encoding suitable mRNA ribosomal binding sites. The ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants may additionally be incorporated. DNA regions are operably linked when they are functionally related to each other. For example, DNA for a signal peptide (secretory leader) is operably linked to DNA for a polypeptide if it is expressed as a precursor which participates in the secretion of the polypeptide; a promoter is operably linked to a coding sequence if it controls the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit translation. Generally, operably linked means contiguous and, in the case of secretory leaders, contiguous and in reading frame. Structural elements intended for use in yeast expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may optionally be subsequently cleaved from the expressed recombinant protein to provide a final product.

DNA sequences encoding mammalian TNF receptors which are to be expressed in a microorganism will preferably contain no introns that could prematurely terminate transcription of DNA into mRNA; however, premature termination of transcription may be desirable, for example, where it would result in mutants having advantageous C-terminal truncations, for example, deletion of a transmembrane region to yield a soluble receptor not bound to the cell membrane. Due to code degeneracy, there can be considerable variation in nucleotide sequences encoding the same amino acid sequence. Other embodiments include sequences capable of hybridizing to the sequences of the provided cDNA under moderately stringent conditions (50°C, 2x SSC) and other sequences hybridizing or degenerate to those which encode biologically active TNF receptor polypeptides.

Recombinant TNFR DNA is expressed or amplified in a recombinant expression system comprising a substantially homogeneous monoculture of suitable host microorganisms, for example, bacteria such as *E. coli* or yeast such as *S. cerevisiae*, which have stably integrated (by transformation or transfection) a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit as a component of a resident plasmid. Generally, cells constituting the system are the progeny of a single ancestral transformant. Recombinant expression systems as defined herein will express heterologous protein upon induction of the regulatory elements linked to the DNA sequence or synthetic gene to be expressed.

Transformed host cells are cells which have been transformed or transfected with TNFR vectors constructed using recombinant DNA techniques. Transformed host cells ordinarily express TNFR, but host cells transformed for purposes of cloning or amplifying TNFR DNA do not need to express TNFR. Expressed TNFR will be deposited in the cell membrane or secreted into the culture supernatant, depending on the TNFR DNA selected. Suitable host cells for expression of mammalian TNFR include prokaryotes, yeast or higher eukaryotic cells under the control of appropriate promoters. Prokaryotes include gram negative or gram positive organisms, for example *E. coli* or bacilli. Higher eukaryotic cells include established cell lines of mammalian origin as described below. Cell-free translation systems could also be employed to produce mammalian TNFR using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pouwels et al. (*Cloning Vectors: A Laboratory Manual*, Elsevier, New York, 1985), the relevant disclosure of which is hereby incorporated by reference.

Prokaryotic expression hosts may be used for expression of TNFR that do not require extensive proteolytic and disulfide processing. Prokaryotic expression vectors generally comprise one or more phenotypic selectable markers, for example a gene encoding proteins conferring antibiotic resistance or supplying an autotrophic requirement, and an origin of replication recognized by the host to ensure amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium*, and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

Useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. *E. coli* is typically transformed using derivatives of pBR322, a plasmid derived from an *E. coli* species (Bolivar et al., *Gene* 2:95, 1977). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells.

Promoters commonly used in recombinant microbial expression vectors include the β -lactamase (penicillinase) and lactose promoter system (Chang et al., *Nature* 275:615, 1978; and Goeddel et al., *Nature* 281:544, 1979), the tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980; and EPA 36,776)

and tac promoter (Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, p. 412, 1982). A particularly useful bacterial expression system employs the phage λ P_L promoter and cI857ts thermolabile repressor. Plasmid vectors available from the American Type Culture Collection which incorporate derivatives of the λ P_L promoter include plasmid pHUB2, resident in *E. coli* strain JMB9 (ATCC 37092) and pPLc28, resident in *E. coli* RR1 (ATCC 53082).

Recombinant TNFR proteins may also be expressed in yeast hosts, preferably from the *Saccharomyces* species, such as *S. cerevisiae*. Yeast of other genera, such as *Pichia* or *Kluyveromyces* may also be employed. Yeast vectors will generally contain an origin of replication from the 2 μ yeast plasmid or an autonomously replicating sequence (ARS), promoter, DNA encoding TNFR, sequences for polyadenylation and transcription termination and a selection gene. Preferably, yeast vectors will include an origin of replication and selectable marker permitting transformation of both yeast and *E. coli*, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 or URA3 gene, which provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, and a promoter derived from a highly expressed yeast gene to induce transcription of a structural sequence downstream. The presence of the TRP1 or URA3 lesion in the yeast host cell genome then provides an effective environment for detecting transformation by growth in the absence of tryptophan or uracil.

Suitable promoter sequences in yeast vectors include the promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073, 1980) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149, 1968; and Holland et al., *Biochem.* 17:4900, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase. Suitable vectors and promoters for use in yeast expression are further described in R. Hitzeman et al., EPA 73,657.

Preferred yeast vectors can be assembled using DNA sequences from pUC18 for selection and replication in *E. coli* (Amp^r gene and origin of replication) and yeast DNA sequences including a glucose-repressible ADH2 promoter and α -factor secretion leader. The ADH2 promoter has been described by Russell et al. (*J. Biol. Chem.* 258:2674, 1982) and Beier et al. (*Nature* 300:724, 1982). The yeast α -factor leader, which directs secretion of heterologous proteins, can be inserted between the promoter and the structural gene to be expressed. See, e.g., Kurjan et al., *Cell* 30:933, 1982; and Bitter et al., *Proc. Natl. Acad. Sci. USA* 81:5330, 1984. The leader sequence may be modified to contain, near its 3' end, one or more useful restriction sites to facilitate fusion of the leader sequence to foreign genes.

Suitable yeast transformation protocols are known to those of skill in the art; an exemplary technique is described by Hinnen et al., *Proc. Natl. Acad. Sci. USA* 75:1929, 1978, selecting for Trp⁺ transformants in a selective medium consisting of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 µg/ml adenine and 20 µg/ml uracil or URA⁺ transformants in medium consisting of 0.67% YNB, with amino acids and bases as described by Sherman et al., *Laboratory Course Manual for Methods in Yeast Genetics*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1986.

Host strains transformed by vectors comprising the ADH2 promoter may be grown for expression in a rich medium consisting of 1% yeast extract, 2% peptone, and 1% or 4% glucose supplemented with 80 µg/ml adenine and 80 µg/ml uracil. Derepression of the ADH2 promoter occurs upon exhaustion of medium glucose. Crude yeast supernatants are harvested by filtration and held at 4°C prior to further purification.

Various mammalian or insect cell culture systems are also advantageously employed to express recombinant protein. Expression of recombinant proteins in mammalian cells is particularly preferred because such proteins are generally correctly folded, appropriately modified and completely functional. Examples of suitable mammalian host cell lines include the COS-7 lines of monkey kidney cells, described by Gluzman (*Cell* 23:175, 1981), and other cell lines capable of expressing an appropriate vector including, for example, L cells, C127, 3T3, Chinese hamster ovary (CHO), HeLa and BHK cell lines. Mammalian expression vectors may comprise nontranscribed elements such as an origin of replication, a suitable promoter and enhancer linked to the gene to be expressed, and other 5' or 3' flanking nontranscribed sequences, and 5' or 3' nontranslated sequences, such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and transcriptional termination sequences. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, *Bio/Technology* 6:47 (1988).

The transcriptional and translational control sequences in expression vectors to be used in transforming vertebrate cells may be provided by viral sources. For example, commonly used promoters and enhancers are derived from Polyoma, Adenovirus 2, Simian Virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites may be used to provide the other genetic elements required for expression of a heterologous DNA sequence. The early and late promoters are particularly useful because both are obtained easily from the virus as a fragment which also contains the SV40 viral origin of replication (Fiers et al., *Nature* 273:113, 1978). Smaller or larger SV40 fragments may also be used, provided

the approximately 250 bp sequence extending from the *Hind* 3 site toward the *Bgl*1 site located in the viral origin of replication is included. Further, mammalian genomic TNFR promoter, control and/or signal sequences may be utilized, provided such control sequences are compatible with the host cell chosen. Additional details regarding the use of a mammalian high expression vector to produce a recombinant mammalian TNF receptor are provided in Examples 2 and 7 below. Exemplary vectors can be constructed as disclosed by Okayama and Berg (*Mol. Cell. Biol.* 3:280, 1983).

A useful system for stable high level expression of mammalian receptor cDNAs in C127 murine mammary epithelial cells can be constructed substantially as described by Cosman et al. (*Mol. Immunol.* 23:935, 1986).

Recombinant expression vectors comprising TNFR cDNAs are stably integrated into a host cell's DNA. Elevated levels of expression product is achieved by selecting for cell lines having amplified numbers of vector DNA. Cell lines having amplified numbers of vector DNA are selected, for example, by transforming a host cell with a vector comprising a DNA sequence which encodes an enzyme which is inhibited by a known drug. The vector may also comprise a DNA sequence which encodes a desired protein. Alternatively, the host cell may be co-transformed with a second vector which comprises the DNA sequence which encodes the desired protein. The transformed or co-transformed host cells are then cultured in increasing concentrations of the known drug, thereby selecting for drug-resistant cells. Such drug-resistant cells survive in increased concentrations of the toxic drug by over-production of the enzyme which is inhibited by the drug, frequently as a result of amplification of the gene encoding the enzyme. Where drug resistance is caused by an increase in the copy number of the vector DNA encoding the inhibitable enzyme, there is a concomitant co-amplification of the vector DNA encoding the desired protein (TNFR) in the host cell's DNA.

A preferred system for such co-amplification uses the gene for dihydrofolate reductase (DHFR), which can be inhibited by the drug methotrexate (MTX). To achieve co-amplification, a host cell which lacks an active gene encoding DHFR is either transformed with a vector which comprises DNA sequence encoding DHFR and a desired protein, or is co-transformed with a vector comprising a DNA sequence encoding DHFR and a vector comprising a DNA sequence encoding the desired protein. The transformed or co-transformed host cells are cultured in media containing increasing levels of MTX, and those cells lines which survive are selected.

A particularly preferred co-amplification system uses the gene for glutamine synthetase (GS), which is responsible for the synthesis of glutamate and ammonia using the hydrolysis of ATP to ADP and phosphate to drive the reaction. GS is subject to inhibition by a variety of inhibitors, for example methionine sulfoximine (MSX). Thus, TNFR can be expressed in high concentrations by co-amplifying cells

transformed with a vector comprising the DNA sequence for GS and a desired protein, or co-transformed with a vector comprising a DNA sequence encoding GS and a vector comprising a DNA sequence encoding the desired protein, culturing the host cells in media containing increasing levels of MSX and selecting for surviving cells. The GS co-amplification system, appropriate recombinant expression vectors and cells lines, are described in the following PCT applications: WO 87/04462, WO 89/01036, WO 89/10404 and WO 86/05807.

Recombinant proteins are preferably expressed by co-amplification of DHFR or GS in a mammalian host cell, such as Chinese Hamster Ovary (CHO) cells, or alternatively in a murine myeloma cell line, such as SP2/0-Ag14 or NS0 or a rat myeloma cell line, such as YB2/3.0-Ag20, disclosed in PCT applications WO/89/10404 and WO 86/05807.

A preferred eukaryotic vector for expression of TNFR DNA is disclosed below in Example 1. This vector, referred to as pCAV/NOT, was derived from the mammalian high expression vector pDC201 and contains regulatory sequences from SV40, adenovirus-2, and human cytomegalovirus.

Purification of Recombinant TNFR

Purified mammalian TNF receptors or analogs are prepared by culturing suitable host/vector systems to express the recombinant translation products of the DNAs of the present invention, which are then purified from culture media or cell extracts.

For example, supernatants from systems which secrete recombinant protein into culture media can be first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. Following the concentration step, the concentrate can be applied to a suitable purification matrix. For example, a suitable affinity matrix can comprise a TNF or lectin or antibody molecule bound to a suitable support. Alternatively, an anion exchange resin can be employed, for example, a matrix or substrate having pendant diethylaminoethyl (DEAE) groups. The matrices can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Alternatively, a cation exchange step can be employed. Suitable cation exchangers include various insoluble matrices comprising sulfopropyl or carboxymethyl groups. Sulfopropyl groups are preferred.

Finally, one or more reversed-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify a TNFR

composition. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a homogeneous recombinant protein.

Recombinant protein produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more concentration, salting-out, aqueous ion exchange or size exclusion chromatography steps. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of recombinant mammalian TNFR can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Fermentation of yeast which express mammalian TNFR as a secreted protein greatly simplifies purification. Secreted recombinant protein resulting from a large-scale fermentation can be purified by methods analogous to those disclosed by Urdal et al. (*J. Chromatog.* 296:171, 1984). This reference describes two sequential, reversed-phase HPLC steps for purification of recombinant human GM-CSF on a preparative HPLC column.

Human TNFR synthesized in recombinant culture is characterized by the presence of non-human cell components, including proteins, in amounts and of a character which depend upon the purification steps taken to recover human TNFR from the culture. These components ordinarily will be of yeast, prokaryotic or non-human higher eukaryotic origin and preferably are present in innocuous contaminant quantities, on the order of less than about 1 percent by weight. Further, recombinant cell culture enables the production of TNFR free of proteins which may be normally associated with TNFR as it is found in nature in its species of origin, e.g. in cells, cell exudates or body fluids.

Therapeutic Administration of Recombinant Soluble TNFR

The present invention provides methods of suppressing TNF-dependent inflammatory responses in humans comprising administering an effective amount of a TNF antagonist, such as TNFR, and a suitable diluent and carrier.

For therapeutic use, purified soluble TNFR protein is administered to a patient, preferably a human, for treatment of arthritis. Thus, for example, soluble TNFR protein compositions can be administered, for example, via intra-articular, intraperitoneal or subcutaneous routes by bolus injection, continuous infusion, sustained release from implants, or other suitable techniques. Typically, a soluble TNFR therapeutic agent will be administered in the form of a composition comprising purified protein in conjunction with physiologically acceptable carriers, excipients or diluents. Such carriers will be nontoxic to recipients at the dosages and concentrations employed. Ordinarily, the preparation of such compositions entails combining the

TNFR with buffers, antioxidants such as ascorbic acid, low molecular weight (less than about 10 residues) polypeptides, proteins, amino acids, carbohydrates including glucose, sucrose or dextrans, chelating agents such as EDTA, glutathione and other stabilizers and excipients. Neutral buffered saline or saline mixed with conspecific serum albumin are exemplary appropriate diluents. Preferably, product is formulated as a lyophilizate using appropriate excipient solutions (e.g., sucrose) as diluents. Appropriate dosages can be determined in trials. In accordance with appropriate industry standards, preservatives may also be added, such as benzyl alcohol. The amount and frequency of administration will depend, of course, on such factors as the nature and severity of the indication being treated, the desired response, the condition of the patient, and so forth.

TNF antagonist proteins are administered to a mammal, preferably a human, for the purpose treating TNF-dependent inflammatory diseases, such as arthritis. For example, TNFRI proteins inhibit TNF-dependent arthritic responses. Because of the primary roles IL-1 and IL-2 play in the production of TNF, combination therapy using TNFR in combination with IL-1R and/or IL-2R may be preferred in the treatment of TNF-associated clinical indications. In the treatment of humans, soluble human TNFR is preferred. Either Type I IL-1R or Type II IL-1R, or a combination thereof, may be used in accordance with the present invention to treat TNF-dependent inflammatory diseases, such as arthritis. Other types of TNF binding proteins may be similarly used.

For treatment of arthritis, TNFR is administered in systemic amounts ranging from about 0.1 mg/kg/week to about 100 mg/kg/week. In preferred embodiments of the present invention, TNFR is administered in amounts ranging from about 0.5 mg/kg/week to about 50 mg/kg/week. For local intra-articular administration, dosages preferably range from about 0.01 mg/kg to about 1.0 mg/kg per injection.

The following examples are offered by way of illustration, and not by way of limitation.

30

EXAMPLES

Example 1

Expression and Purification of Soluble Human TNFRI

35

The cloning of the cDNA for the 80 kD form of the human TNF receptor has been described in detail (Smith et al., *Science* 248:1019, 1990). The expression vector pCAV/NOT-TNFR (ATCC 68088) containing the TNFR cDNA clone 1 was used to prepare and express a soluble human TNFRI as follows.

A cDNA encoding a soluble human TNFRIΔ235 (the primary translation product of which had the sequence of amino acids -22-235 of SEQ ID NO:1) was constructed by excising an 840 bp fragment from pCAV/NOT-TNFR with the restriction enzymes Not1 and Pvu2. Not1 cuts at the multiple cloning site of pCAV/NOT-TNFR and Pvu2 cuts within the TNFR coding region 20 nucleotides 5' of the transmembrane region. In order to reconstruct the 3' end of the TNFR sequences, two oligonucleotides were synthesized and annealed to create the following oligonucleotide linker encoding amino acids corresponding to amino acids 229-235 of SEQ ID NO:1:

```

Pvu2                               BamH1 Bgl2
CTGAAGGGAGCACTGGCGACTTAAGGATCCA
GACTTCCCTCGTGACCGCTGATTCCTAGGTCTAG
AlaGluGlySerThrGlyAspEnd

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This oligonucleotide linker has terminal Pvu2 and Bgl2 restriction sites, regenerates 20 nucleotides of the TNFR, followed by a termination codon (underlined) and a BamH1 restriction site (for convenience in isolating the entire soluble TNFR by Not1/BamH1 digestion). This oligonucleotide was then ligated with the 840 bp Not1/Pvu2 TNFR insert into Bgl2/Not1 cut pCAV/NOT to yield psolhuTNFRIΔ235/CAVNOT, which was transfected into COS-7 cells as described above. The host cells expressed a mature soluble human TNFRI protein having the sequence of amino acids 1-235 which was capable of binding TNF.

Example 2

Construction and Expression of Soluble Human TNFR/Fc Fusion Protein

A schematic diagram showing the construction of a recombinant soluble human TNFR:Fc expression vector is shown in Figure 1. The rhu TNFR:Fc fusion gene was created by ligating the following fragments into Bluescript®, a commercially available cloning vector (Stratagene):

1) An 867 bp Asp718-Pvu2 fragment from pCAV/NOT-TNFR (ATCC 68088) containing the cDNA encoding the truncated TNFR.

2) A 700 bp Styl-Spel fragment from plasmid pIXY498 coding for 232 amino acids of the Fc portion of human IgG1. Plasmid pIXY498 is a yeast expression vector containing the Fc fragment of human IgG1 (see Figure 2).

3) An oligonucleotide linker, to fuse the truncated TNFR with the human IgG1 Fc fragment. This linker was created by PCR (polymerase chain reaction) amplification using two primers, one having the sequence
 CCCCAGCTGAAGGGAGCACTGGCG
 5 ACGAGCCCAAATCTTGTGACAAACTC (nucleotides 833-883 of SEQ ID NO: 3) which encodes the 3' end of the truncated TNF receptor and the 5' end of human IgG1, and the other having the sequence
 CCGTACGTGCTGTTGTTACTGC (SEQ ID NO:5), an antisense sequence encoding nucleotides 257-237 of human IgG1. The template for this reaction
 10 was pIXY498. The reaction product was digested with Pvu2 and Sty1, and a 115 bp fragment was isolated.

This construct was then digested with Not1 and the resulting 1.4 kilobase fragment containing the rhu TNFR:Fc fusion DNA sequence was ligated into the Not1
 15 site of plasmid CAV/NOT/DHFR. Plasmid pCAV/NOT/DHFR was derived from plasmid pCAV/NOT by inserting the hamster dihydrofolate reductase DNA sequence (DHFR) into the Hpa1 site of pCAV/NOT (Figure 2). This construct was designated plasmid pCAVDHFRhuTNFRFc. The entire coding region sequence was confirmed by DNA sequencing and is depicted in Figure 2.

20 To prepare the host strain, DXB-11 CHO cells deficient in the expression of dihydrofolate reductase (DHFR) were obtained from Dr. Lawren Chasin at Columbia University. A bank of 100 vials of these cells was established, and representative vials were sent to Microbiological Associates for examination via the following procedures:

25	<u>Test</u>	<u>Result</u>
	1. Transmission Electron Microscopy (TEM)	Type A only,
	2. Sterility - Bacterial and Fungal	negative
	3. Mycoplasma	negative
	4. Mouse Antibody Production (MAP)	negative

30

All transfections and amplification steps were performed in a separate laboratory set aside for this purpose. Only mycoplasma-free cell lines were allowed into this facility.

Transfections were performed by mixing pCAVDHFRhuTNFRFc plasmid
 35 DNA with LipofectinTM reagent from Gibco BRL. Approximately 10 µg of DNA was added to 10 cm petri dishes containing CHO DXB-11 cells. After the initial transfection, cells were selected for the expression of DHFR by subculturing in selective medium lacking glycine, hypoxanthine and thymidine. The resulting colonies

were then transferred to 24 well plates and analyzed for rhu TNFR:Fc expression. The highest expressing cultures were subjected to amplification by exposure to increasing concentrations of methotrexate (MTX). Cells able to grow at 25 nM MTX were cloned by limiting dilution in 96 well plates. The highest expressing clones were transferred to
5 suspension culture and the final selection of clone 4-4FC102A5-3 was made based on its high level of rhu TNFR:Fc expression under these conditions.

Example 3

Expression of Monomeric Soluble TNF Receptors in CHO Cells

10

Soluble TNF receptor was expressed in Chinese Hamster Ovary (CHO) cells using the glutamine-synthetase (GS) gene amplification system, substantially as described in PCT patent application Nos. WO87/04462 and WO89/01036. Briefly, CHO cells are transfected with an expression vector containing genes for both TNFR and GS. CHO cells are selected for GS gene expression based on the ability of the
15 transfected DNA to confer resistance to low levels of methionine sulfoximine (MSX). GS sequence amplification events in such cells are selected using elevated MSX concentrations. In this way, contiguous TNFR sequences are also amplified and enhanced TNFR expression is achieved.

20

The vector used in the GS expression system was pSolTNFR/P6/PSVLGS, which was constructed as follows. First, the vector pSVLGS.1 (described in PCT Application Nos. WO87/04462 and WO89/01036, and available from Celltech, Ltd., Berkshire, UK) was cut with the BamH1 restriction enzyme and dephosphorylated with calf intestinal alkaline phosphatase (CIAP) to prevent the vector from religating to
25 itself. The BamH1 cut pSVLGS.1 fragment was then ligated to a 2.4 kb BamH1 to Bgl2 fragment of pEE6hCMV (described in PCT Application No. WO89/01036, also available from Celltech) which was cut with Bgl2, BamH1 and Fsp1 to avoid two fragments of similar size, to yield an 11.2 kb vector designated p6/PSVLGS.1. pSVLGS.1 contains the glutamine synthetase selectable marker gene under control of the SV40 later promoter. The BamH1 to Bgl2 fragment of pEE6hCMV contains the
30 human cytomegalovirus major immediate early promoter (hCMV), a polylinker, and the SV40 early polyadenylation signal. The coding sequences for soluble TNFR were added to p6/PSVLGS.1 by excising a Not1 to BamH1 fragment from the expression vector pSolTNFR/CAVNOT (made according to Example 3 above), blunt ending with
35 Klenow and ligating with SmaI cut dephosphorylated p6/PSVLGS.1, thereby placing the SolTNFR coding sequences under the control of the hCMV promoter. This resulted in a single plasmid vector in which the SV40/GS and hCMB/SolTNFR transcription

units are transcribed in opposite directions. This vector was designated psolTNFR/P6/PSVLGS.

psolTNFR/P6/PSVLGS was used to transfect CHO-K1 cells (available from ATCC, Rockville, MD, under accession number CCL 61) as follows. A monolayer of
5 CHO-K1 cells were grown to subconfluency in Minimum Essential Medium (MEM) 10X (Gibco: 330-1581AJ) without glutamine and supplemented with 10% dialysed fetal bovine serum (Gibco: 220-6300AJ), 1 mM sodium pyruvate (Sigma), MEM non-essential amino acids (Gibco: 320-1140AG), 500 μ M asparagine and glutamate (Sigma) and nucleosides (30 μ M adenosine, guanosine, cytidine and uridine and 10 μ M
10 thymidine)(Sigma).

Approximately 1×10^6 cells per 10 cm petri dish were transfected with 10 μ g of psolTNFR/P6/PSVLGS by standard calcium phosphate precipitation, substantially as described by Graham & van der Eb, *Virology* 52:456 (1983). Cells were subjected to glycerol shock (15% glycerol in serum-free culture medium for approximately 1.5
15 minutes) approximately 4 hours after transfection, substantially as described by Frost & Williams, *Virology* 91:39 (1978), and then washed with serum-free medium. One day later, transfected cells were fed with fresh selective medium containing MSX at a final concentration of 25 μ M. Colonies of MSX-resistant surviving cells were visible within
20 to confluency in selective medium. Conditioned medium from confluent wells were then assayed for soluble TNFR activity using standard binding assays. These assays indicated that the colonies expressed biologically active soluble TNFR.

In order to select for GS gene amplification, several MSX-resistant cell lines are transfected with psolTNFR/P6/PSVLGS and grown in various concentrations of MSX.
25 For each cell line, approximately 1×10^6 cells are plated in gradually increasing concentrations of 100 μ M, 250 μ M, 500 μ M and 1 mM MSX and incubated for 10-14 days. After 12 days, colonies resistant to the higher levels of MSX appear. The surviving colonies are assayed for TNFR activity. Each of these highly resistant cell lines contains cells which arise from multiple independent amplification events. From
30 these cells lines, one or more of the most highly resistant cells lines are isolated. The amplified cells with high production rates are then cloned by limiting dilution cloning. Mass cell cultures of the transfectants secrete active soluble TNFR.

Example 4

35 Effect of Soluble TNFR on Antigen-Induced Arthritis in Rats

Lewis rats previously immunized with methylated bovine serum albumin (mBSA) in complete Freund's adjuvant develop antigen-induced arthritis (AIA) when

challenged with mBSA in knee joints. Administration of rhu TNFR:Fc, TNFR monomer, recombinant murine soluble IL-1 receptor (rm IL-1R) or a combination of TNFR monomer plus rm IL-1R was shown to be effective in suppressing the effects of antigen-induced arthritis in rats.

- 5 Lewis rats were immunized in the hind flank with 0.5 mg mBSA in complete Freund's adjuvant. Twenty-one days later (day 0), the animals were injected in both hind knee joints with 50 µg mBSA in pyrogen-free saline. Groups of six rats were injected intra-articularly in both knee joints on that day and on the following 2 days (days 0, 1 and 2) as indicated below in Table A:

10

Table A
Treatment and Dosage Schedule

	Group	Treatment	Dose
15			
	1	rhu TNFR/Fc	10 µg
	2	rhu TNFR/Fc	5 µg
	3	rmu IL-1 Receptor	1 µg
20	4	TNFR Monomer	5 µg
	5	TNFR Monomer/rmu IL-1R	10 µg/1 µg
	6	Diluent (saline)	-

- 25 Knee joint width was measured daily on days 0-6 relative to treatment. TNFR monomer was produced in CHO cells according to Example 2. The rhu TNFR:Fc used in this experiment was produced in BHK (hamster kidney) cells. This material is similar to the CHO cell-derived TNFR.

- 30 Figures 3 and 4 demonstrate that treatment with BHK-derived rhu TNFR:Fc at the time of mBSA challenge and for two days following challenge resulted in a reduction of knee-joint swelling in comparison to diluent-treated control rats. A reduction in joint swelling and inflammation was observed in rats treated with 5 or 10 µg BHK-derived rhu TNFR:Fc or 5 µg TNFR monomer or 1 µg of rmuIL-1R. Reduction in joint swelling was even more pronounced when rmuIL-1R and TNFR monomer treatment was combined.

- 35 Histopathological examination of the joints harvested on day 6 was performed to confirm the degree of swelling. Histopathology scores were derived by evaluating knee joints and scoring their condition as follows: Grade 1, minimal, <10% of area

affected; Grade 2, moderate, 10-50% of area affected; Grade 3, marked, at least 50%, but less than all, of area affected; Grade 4, maximal, total area severely affected. A variety of lesions/alterations involving five knee joint structures were evaluated: joint capsule, joint space, synovial membrane, articular cartilage, and subchondral bone.

- 5 Each structural alteration was scored from 1 to 4, and the scores were added and means were calculated. Histopathology results are expressed as the mean score in each treatment group.

The following Table B shows histopathology results, which also indicate that rhu TNFR:Fc, TNFR monomer and rmu IL-1R were effective in reducing the severity of antigen-induced arthritis, and that a combination of rm IL-1R and TNFR monomer was more effective than either receptor alone.

Table B
Effect of rhu TNFR:Fc on Antigen Induced Arthritis in Rats

15	Treatment	Histopathology Score (Mean \pm SD (SE))	Number Of Animals
20	Saline	18.4 \pm 4.9 (1.5)	10
	1.0 μ g rmu IL-1R	13.1 \pm 4.7 (1.7)	8
	10.0 μ g TNFR monomer	12.8 \pm 3.1 (1.1)	8
	1.0 μ g rmu IL-1R/10.0 μ g TNFR monomer	7.9 \pm 5.2 (2.0)	5
25	5.0 μ g TNFR monomer	13.4 \pm 2.8 (1.0)	9
	5.0 μ g rhu TNFR:Fc (BHK)	13.4 \pm 3.6 (1.3)	8

In summary, treatment with rhu TNFR/Fc, TNFR monomer, or rmu IL-1R at the time of mBSA challenge and for two days following challenge resulted in a reduction of knee-joint swelling in comparison to diluent-treated control rats. A combination of both rmu IL-1R and TNFR monomer resulted in greater reduction of swelling than either receptor molecule alone. Histopathology results also indicated that rhu TNFR/Fc, TNFR and rmu IL-1R were effective in reducing the severity of antigen-induced arthritis, and that a combination of rmu IL-1R and TNFR monomer was more effective than either receptor alone.

Example 5**Effect of Soluble TNFR on Collagen-Induced Arthritis in B10.RIII Mice**

B10.RIII mice previously immunized with porcine type II collagen (CII) in complete Freund's adjuvant consistently develop collagen-induced arthritis (CIA). Administration of rhu TNFR:Fc was shown to be effective in suppressing the symptoms of CIA in mice.

B10.RIII mice were immunized intradermally with 100 µg porcine type II collagen (CII) in complete Freund's adjuvant to induced arthritic symptoms. Approximately 14-17 days post-immunization, symptoms of clinical arthritis began to appear in the mice, with 90-100% of the mice displaying severe arthritis by day 28. Mice were injected intraperitoneally with TNFR/Fc or PBS to determine the effect of soluble TNFR/Fc on CIA. Mice were assessed for symptoms of arthritis at 12 weeks post-immunization.

In a first experiment, TNFR/Fc was administered over the entire period of CIA development. Twelve mice were injected with 10 µg TNFR/Fc, 3 days per week, from days 0 to 35. Twelve control mice were injected with PBS. Figure 5 shows that TNFR/Fc significantly reduced the incidence of arthritis when compared to controls. Upon cessation of treatment with TNFR/Fc, the mice developed arthritis.

In a second experiment, TNFR/Fc was administered during only the developmental stages of CIA on days -1-17 relative to immunization, as set forth in the following Table C.

Table C**Effect of rhu TNFR:Fc Administered During Inductive Stage of CIA**

Treatment	Incidence (Positive/Total)	Onset (Mean Day \pm SE)	Severity (Mean \pm SE)
30 µg TNFR/Fc Days -1, 3	10/10	24 \pm 2	10.5 \pm 0.5
10 µg TNFR/Fc Days -1 to 17 (alternate days)	8/10	21 \pm 2	8.6 \pm 0.6
100 µl PBS Days -1 to 17 (alternate days)	10/10	18 \pm 1	10.6 \pm 0.4

These data show that TNFR/Fc delayed the onset of arthritis, but that CIA was unaltered in mice receiving 30 μ g TNFR/Fc the day before and 3 days after immunization with type II collagen. Mice given 10 μ g TNFR/Fc, every other day, from day -1 to day 17 displayed a slight decrease in CIA incidence and severity versus controls injected with PBS.

In a third experiment, TNFR/Fc was administered during only the progressive stages of CIA every other day on days 14-28 post-immunization as set forth in the following Table D.

Table D
Effect of rhu TNFR:Fc Administered During Progressive Stage of CIA

Treatment	Incidence (Positive/Total)	Onset (Mean Day \pm SE)	Severity (Mean \pm SE)
10 μ g TNFR/Fc Days 14-28 (alternate days)	8/9	27 \pm 6	8.6 \pm 1.3
100 μ l PBS Days 14-28 (alternate days)	9/9	21 \pm 1	8.7 \pm 0.6

These data show that mice given 10 μ g TNFR/Fc, every other day, from days 14-28 showed a slight delay in CIA onset when compared to control animals. However, the incidence and severity of arthritis appears to be unaltered.

In summary, these experiments indicate that TNFR/Fc was effective in delaying the onset of CIA when administered over the entire course of CIA development.

Example 6

Effect of Soluble TNFR on Collagen-Induced Arthritis in DBA/1 Mice

The effect of soluble TNFR/Fc on CIA in DBA/1 mice previously immunized with porcine type II collagen (CII) in complete Freund's adjuvant was also tested. Administration of rhu TNFR:Fc was shown to be effective in suppressing the symptoms of CIA.

In this experiment, DBA/1 mice were immunized with 100 μ g of CII and then injected intraperitoneally with 50 μ g recombinant soluble human TNFR/Fc in sterile saline from day 21 to day 28. Control mice received sterile saline (vehicle) injections.

This treatment period was prior to the development of the clinical signs of CIA, but during the development of DTH responses to type II collagen and rapid IgG anti-CII production.

Both groups of mice were assessed for the development of CIA for 70 days, and onset of CIA for 44-55 days post-immunization. Figures 6 and 7 show that TNFR/Fc significantly reduced the incidence of CIA compared with controls (28% vs. 86%; $p < 0.03$), and reduced both arthritis index (a subjective measure of severity) and the number of involved joints. The antibody response to CII was significantly lower immediately post treatment with TNFR/Fc (day 28), but antibody levels were equivalent at the conclusion of the experiment (day 70).

These results indicate that TNFR/Fc is effective in reducing the incidence of CIA in mice and may therefore be useful in the treatment arthritis.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Jacobs, Cindy A.

(ii) TITLE OF INVENTION: Method of Treating TNF-Dependent
Inflammation Using Tumor Necrosis Factor Antagonists

10

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

15

(A) ADDRESSEE: Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: U.S.A.
(F) ZIP: 98101

20

(v) COMPUTER READABLE FORM:

25

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

30

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

35

(A) NAME: Wight, Christopher L.
(B) REGISTRATION NUMBER: 31,680
(C) REFERENCE/DOCKET NUMBER: 2503

(ix) TELECOMMUNICATION INFORMATION:

40

(A) TELEPHONE: (206) 587-0430
(B) TELEFAX: (206) 587-0606

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1641 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

55

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Homo sapiens
(G) CELL TYPE: Fibroblast
(H) CELL LINE: WI-26 VA4

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: WI-26 VA4
 (B) CLONE: Clone 1

5 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 88..1473

10 (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 154..1470

15 (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 88..153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20	GCGAGGCAGG CAGCCTGGAG AGAAGGCGCT GGGCTGCGAG GCGCGAGGG CGCGAGGGCA	60
	GGGGGCAACC GGACCCCGCC CGCATCC ATG GCG CCC GTC GCC GTC TGG GCC	111
	Met Ala Pro Val Ala Val Trp Ala	
	-22 -20 -15	
25	GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC	159
	Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro	
	-10 -5 1	
30	GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC	207
	Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys	
	5 10 15	
35	CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA	255
	Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys	
	20 25 30	
40	TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC	303
	Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp	
	35 40 45 50	
45	ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC	351
	Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn	
	55 60 65	
50	TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG	399
	Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln	
	70 75 80	
55	GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC	447
	Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys	
	85 90 95	
60	AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG CTG	495
	Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu	
	100 105 110	
60	TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC AGA CCA	543
	Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro	
	115 120 125 130	

29

		GGA	ACT	GAA	ACA	TCA	GAC	GTG	GTG	TGC	AAG	CCC	TGT	GCC	CCG	GGG	ACG	591
		Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	
						135					140					145		
5		TTC	TCC	AAC	ACG	ACT	TCA	TCC	ACG	GAT	ATT	TGC	AGG	CCC	CAC	CAG	ATC	639
		Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	
					150					155					160			
10		TGT	AAC	GTG	GTG	GCC	ATC	CCT	GGG	AAT	GCA	AGC	ATG	GAT	GCA	GTC	TGC	687
		Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	
				165					170					175				
15		ACG	TCC	ACG	TCC	CCC	ACC	CGG	AGT	ATG	GCC	CCA	GGG	GCA	GTA	CAC	TTA	735
		Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	Gly	Ala	Val	His	Leu	
			180					185					190					
20		CCC	CAG	CCA	GTG	TCC	ACA	CGA	TCC	CAA	CAC	ACG	CAG	CCA	ACT	CCA	GAA	783
		Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	
		195					200					205					210	
		CCC	AGC	ACT	GCT	CCA	AGC	ACC	TCC	TTC	CTG	CTC	CCA	ATG	GGC	CCC	AGC	831
		Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	
						215					220					225		
25		CCC	CCA	GCT	GAA	GGG	AGC	ACT	GGC	GAC	TTC	GCT	CTT	CCA	GTT	GGA	CTG	879
		Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	
					230					235					240			
30		ATT	GTG	GGT	GTG	ACA	GCC	TTG	GGT	CTA	CTA	ATA	ATA	GGA	GTG	GTG	AAC	927
		Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	
				245					250					255				
35		TGT	GTC	ATC	ATG	ACC	CAG	GTG	AAA	AAG	AAG	CCC	TTG	TGC	CTG	CAG	AGA	975
		Cys	Val	Ile	Met	Thr	Gln	Val	Lys	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	
			260					265					270					
40		GAA	GCC	AAG	GTG	CCT	CAC	TTG	CCT	GCC	GAT	AAG	GCC	CGG	GGT	ACA	CAG	1023
		Glu	Ala	Lys	Val	Pro	His	Leu	Pro	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	
		275					280					285					290	
		GGC	CCC	GAG	CAG	CAG	CAC	CTG	CTG	ATC	ACA	GCG	CCG	AGC	TCC	AGC	AGC	1071
		Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	
						295					300					305		
45		AGC	TCC	CTG	GAG	AGC	TCG	GCC	AGT	GCG	TTG	GAC	AGA	AGG	GCG	CCC	ACT	1119
		Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	
					310					315					320			
50		CGG	AAC	CAG	CCA	CAG	GCA	CCA	GGC	GTG	GAG	GCC	AGT	GGG	GCC	GGG	GAG	1167
		Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	
				325					330					335				
55		GCC	CGG	GCC	AGC	ACC	GGG	AGC	TCA	GAT	TCT	TCC	CCT	GGT	GGC	CAT	GGG	1215
		Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	
			340					345					350					
60		ACC	CAG	GTC	AAT	GTC	ACC	TGC	ATC	GTG	AAC	GTC	TGT	AGC	AGC	TCT	GAC	1263
		Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	
		355					360					365					370	

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CAC AGC TCA CAG TGC TCC TCC CAA GCC AGC TCC ACA ATG GGA GAC ACA 1311
 His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr 385
 375 380 385
 5 GAT TCC AGC CCC TCG GAG TCC CCG AAG GAC GAG CAG GTC CCC TTC TCC 1359
 Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val Pro Phe Ser 400
 390 395 400
 10 AAG GAG GAA TGT GCC TTT CGG TCA CAG CTG GAG ACG CCA GAG ACC CTG 1407
 Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro Glu Thr Leu 415
 405 410 415
 CTG GGG AGC ACC GAA GAG AAG CCC CTG CCC CTT GGA GTG CCT GAT GCT 1455
 Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala 430
 420 425 430
 15 GGG ATG AAG CCC AGT TAACCAGGCC GGTGTGGGCT GTGTCGTAGC CAAGGTGGGC 1510
 Gly Met Lys Pro Ser 440
 435 440
 20 TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCCC CCACCACTAG 1570
 GACTCTGAGG CTCTTTCTGG GCCAAGTTCC TCTAGTGCCC TCCACAGCCG CAGCCTCCCT 1630
 25 CTGACCTGCA G 1641

(2) INFORMATION FOR SEQ ID NO:2:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 40 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 -22 -20 -15 -10
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 -5 1 5 10
 45 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 15 20 25
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 30 35 40
 50 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 45 50 55
 55 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 60 65 70
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 75 80 85 90
 60 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 95 100 105

	Ser	Lys	Gln	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	
				110					115					120			
5	Pro	Gly	Phe	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	
			125					130					135				
	Cys	Lys	Pro	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	
		140					145					150					
10	Asp	Ile	Cys	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	
	155					160					165					170	
	Asn	Ala	Ser	Met	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	
15					175					180					185		
	Met	Ala	Pro	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	
				190					195					200			
20	Gln	His	Thr	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	
			205					210					215				
	Phe	Leu	Leu	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	
	220						225					230					
25	Asp	Phe	Ala	Leu	Pro	Val	Gly	Leu	Ile	Val	Gly	Val	Thr	Ala	Leu	Gly	
	235					240					245					250	
	Leu	Leu	Ile	Ile	Gly	Val	Val	Asn	Cys	Val	Ile	Met	Thr	Gln	Val	Lys	
30					255					260					265		
	Lys	Lys	Pro	Leu	Cys	Leu	Gln	Arg	Glu	Ala	Lys	Val	Pro	His	Leu	Pro	
				270					275					280			
35	Ala	Asp	Lys	Ala	Arg	Gly	Thr	Gln	Gly	Pro	Glu	Gln	Gln	His	Leu	Leu	
			285					290					295				
	Ile	Thr	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Glu	Ser	Ser	Ala	Ser	
	300						305					310					
40	Ala	Leu	Asp	Arg	Arg	Ala	Pro	Thr	Arg	Asn	Gln	Pro	Gln	Ala	Pro	Gly	
	315					320					325					330	
	Val	Glu	Ala	Ser	Gly	Ala	Gly	Glu	Ala	Arg	Ala	Ser	Thr	Gly	Ser	Ser	
45					335					340					345		
	Asp	Ser	Ser	Pro	Gly	Gly	His	Gly	Thr	Gln	Val	Asn	Val	Thr	Cys	Ile	
				350				355						360			
50	Val	Asn	Val	Cys	Ser	Ser	Ser	Asp	His	Ser	Ser	Gln	Cys	Ser	Ser	Gln	
		365						370					375				
	Ala	Ser	Ser	Thr	Met	Gly	Asp	Thr	Asp	Ser	Ser	Pro	Ser	Glu	Ser	Pro	
	380						385					390					
55	Lys	Asp	Glu	Gln	Val	Pro	Phe	Ser	Lys	Glu	Glu	Cys	Ala	Phe	Arg	Ser	
	395					400					405					410	
	Gln	Leu	Glu	Thr	Pro	Glu	Thr	Leu	Leu	Gly	Ser	Thr	Glu	Glu	Lys	Pro	
60					415					420					425		

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
430 435

5 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- 20 (B) CLONE: TNFR/Fc Fusion Protein

(ix) FEATURE:

- 25 (A) NAME/KEY: CDS
(B) LOCATION: 1..1557

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
(B) LOCATION: 1..1554

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	GCG AGG CAG GCA GCC TGG AGA GAA GGC GCT GGG CTG CGA GGG CGC GAG	48
35	Ala Arg Gln Ala Ala Trp Arg Glu Gly Ala Gly Leu Arg Gly Arg Glu	
	1 5 10 15	
	GGC GCG AGG GCA GGG GGC AAC CGG ACC CCG CCC GCA TCC ATG GCG CCC	96
	Gly Ala Arg Ala Gly Gly Asn Arg Thr Pro Pro Ala Ser Met Ala Pro	
40	20 25 30	
	GTC GCC GTC TGG GCC GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG	144
	Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala	
	35 40 45	
45	GCG CAC GCC TTG CCC GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG	192
	Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu	
	50 55 60	
	CCC GGG AGC ACA TGC CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG	240
50	Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln	
	65 70 75 80	
	ATG TGC TGC AGC AAA TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT	288
55	Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys	
	85 90 95	
	ACC AAG ACC TCG GAC ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC	336
	Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr	
60	100 105 110	

33

	ACC CAG CTC TGG AAC TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC	384
	Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg	
	115 120 125	
5	TGT AGC TCT GAC CAG GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC	432
	Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn	
	130 135 140	
10	CGC ATC TGC ACC TGC AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG	480
	Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln	
	145 150 155 160	
15	GAG GGG TGC CGG CTG TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC	528
	Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe	
	165 170 175	
	GGC GTG GCC AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC	576
	Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro	
	180 185 190	
20	TGT GCC CCG GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC	624
	Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys	
	195 200 205	
25	AGG CCC CAC CAG ATC TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC	672
	Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser	
	210 215 220	
30	ATG GAT GCA GTC TGC ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA	720
	Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro	
	225 230 235 240	
	GGG GCA GTA CAC TTA CCC CAG CCA GTG TCC ACA CGA TCC CAA CAC ACG	768
	Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr	
	245 250 255	
35	CAG CCA ACT CCA GAA CCC AGC ACT GCT CCA AGC ACC TCC TTC CTG CTC	816
	Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu	
	260 265 270	
40	CCA ATG GGC CCC AGC CCC CCA GCT GAA GGG AGC ACT GGC GAC GAG CCC	864
	Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Glu Pro	
	275 280 285	
45	AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT GAA	912
	Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu	
	290 295 300	
50	CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC	960
	Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp	
	305 310 315 320	
	ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC	1008
	Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp	
	325 330 335	
55	GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC	1056
	Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly	
	340 345 350	

34

	GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC	1104
	Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn	
	355 360 365	
5	AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG	1152
	Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp	
	370 375 380	
10	CTG AAT GGC AAG GAC TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA	1200
	Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro	
	385 390 395 400	
15	GCC CCC ATG CAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA	1248
	Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	
	405 410 415	
20	CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC AAG AAC	1296
	Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn	
	420 425 430	
25	CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGG CAC ATC	1344
	Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile	
	435 440 445	
30	GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC	1392
	Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	
	450 455 460	
35	ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG	1440
	Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	
	465 470 475 480	
40	CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC	1488
	Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	
	485 490 495	
45	TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC	1536
	Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu	
	500 505 510	
50	TCC CTG TCT CCG GGT AAA TGA	1557
	Ser Leu Ser Pro Gly Lys	
	515	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Arg Gln Ala Ala Trp Arg Glu Gly Ala Gly Leu Arg Gly Arg Glu
1 5 10 15
Gly Ala Arg Ala Gly Gly Asn Arg Thr Pro Pro Ala Ser Met Ala Pro
20 25 30

35

	Val	Ala	Val	Trp	Ala	Ala	Leu	Ala	Val	Gly	Leu	Glu	Leu	Trp	Ala	Ala	
			35					40					45				
5	Ala	His	Ala	Leu	Pro	Ala	Gln	Val	Ala	Phe	Thr	Pro	Tyr	Ala	Pro	Glu	
		50					55					60					
	Pro	Gly	Ser	Thr	Cys	Arg	Leu	Arg	Glu	Tyr	Tyr	Asp	Gln	Thr	Ala	Gln	
		65				70					75					80	
10	Met	Cys	Cys	Ser	Lys	Cys	Ser	Pro	Gly	Gln	His	Ala	Lys	Val	Phe	Cys	
					85					90					95		
	Thr	Lys	Thr	Ser	Asp	Thr	Val	Cys	Asp	Ser	Cys	Glu	Asp	Ser	Thr	Tyr	
15				100					105					110			
	Thr	Gln	Leu	Trp	Asn	Trp	Val	Pro	Glu	Cys	Leu	Ser	Cys	Gly	Ser	Arg	
			115					120					125				
20	Cys	Ser	Ser	Asp	Gln	Val	Glu	Thr	Gln	Ala	Cys	Thr	Arg	Glu	Gln	Asn	
		130					135					140					
	Arg	Ile	Cys	Thr	Cys	Arg	Pro	Gly	Trp	Tyr	Cys	Ala	Leu	Ser	Lys	Gln	
25		145				150					155					160	
	Glu	Gly	Cys	Arg	Leu	Cys	Ala	Pro	Leu	Arg	Lys	Cys	Arg	Pro	Gly	Phe	
				165						170					175		
	Gly	Val	Ala	Arg	Pro	Gly	Thr	Glu	Thr	Ser	Asp	Val	Val	Cys	Lys	Pro	
30				180					185					190			
	Cys	Ala	Pro	Gly	Thr	Phe	Ser	Asn	Thr	Thr	Ser	Ser	Thr	Asp	Ile	Cys	
			195					200					205				
35	Arg	Pro	His	Gln	Ile	Cys	Asn	Val	Val	Ala	Ile	Pro	Gly	Asn	Ala	Ser	
		210					215					220					
	Met	Asp	Ala	Val	Cys	Thr	Ser	Thr	Ser	Pro	Thr	Arg	Ser	Met	Ala	Pro	
40		225				230					235					240	
	Gly	Ala	Val	His	Leu	Pro	Gln	Pro	Val	Ser	Thr	Arg	Ser	Gln	His	Thr	
				245						250					255		
	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Pro	Ser	Thr	Ser	Phe	Leu	Leu	
45				260					265					270			
	Pro	Met	Gly	Pro	Ser	Pro	Pro	Ala	Glu	Gly	Ser	Thr	Gly	Asp	Glu	Pro	
			275					280					285				
50	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
		290					295					300					
	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	
55		305				310					315					320	
	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
				325						330					335		
	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
60				340					345					350			

36

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 355 360 365

5 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 370 375 380

Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 385 390 395 400

10 Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 405 410 415

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 420 425 430

15 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile
 435 440 445

20 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 450 455 460

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 465 470 475 480

25 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 485 490 495

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 500 505 510

30 Ser Leu Ser Pro Gly Lys
 515

35 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

45 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

50 (vii) IMMEDIATE SOURCE:
 (B) CLONE: oligonucleotide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
 CGGTACGTGC TGTTGTTACT GC

CLAIMS

We claim:

5

1. A method for treating TNF-mediated inflammatory diseases which comprises administering to a mammal in need thereof a therapeutically effective amount of a TNF antagonist.

10

2. A method according to claim 1, wherein the TNF-mediated inflammatory disease is arthritis.

3. A method according to claim 2, wherein the mammal is a human.

15

4. A method according to claim 3, wherein the TNF antagonist is soluble human TNFR.

20

5. A method according to claim 4, wherein the soluble human TNFR is selected from the group consisting of soluble human Type I TNFR and soluble human Type II TNFR.

6. A method according to claim 4, wherein the soluble human TNFR is fused to the Fc region of a human immunoglobulin molecule.

25

7. A method according to claim 2, wherein TNFR is administered in combination with IL-1R.

30

8. A method for treating arthritis in a mammal, comprising the step of administering to a mammal having arthritis an amount of soluble human TNFR ranging from about 0.1 mg/kg/week to about 100 mg/kg/week.

9. A method according to claim 8, wherein the amount of soluble human TNFR ranges from about 0.5 mg/kg/week to about 50 mg/kg/week.

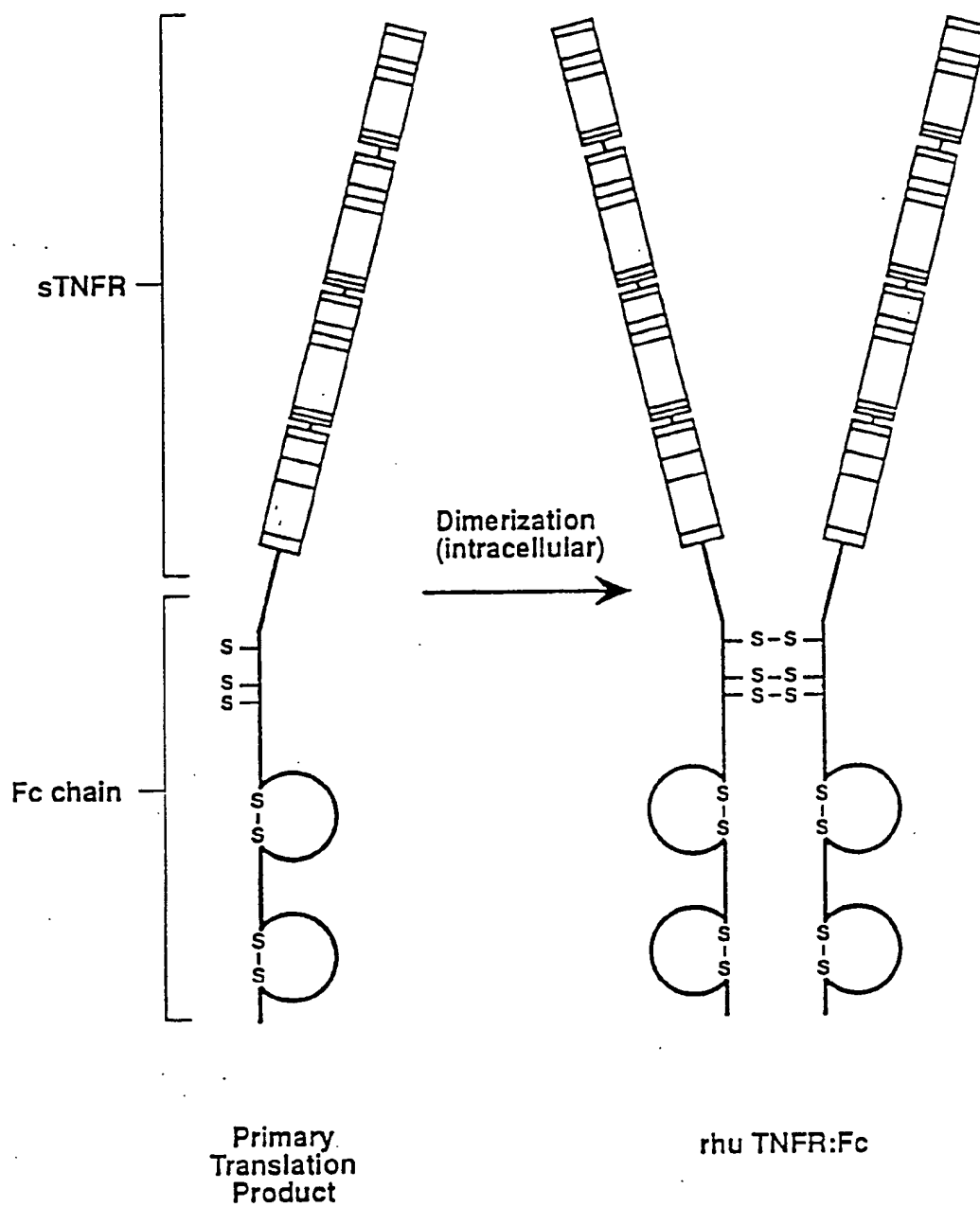


FIGURE 1

2 / 6

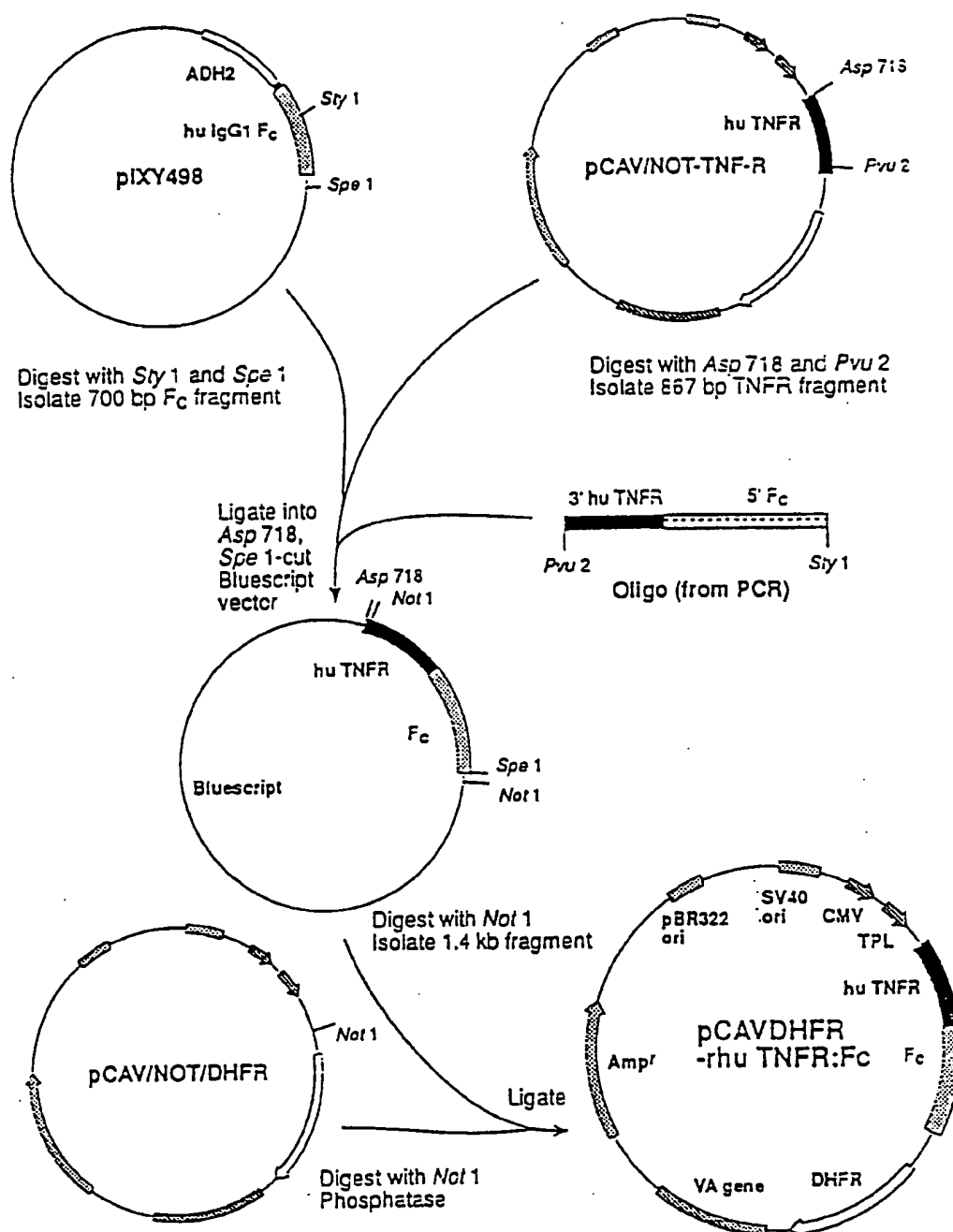


FIGURE 2

3 / 6

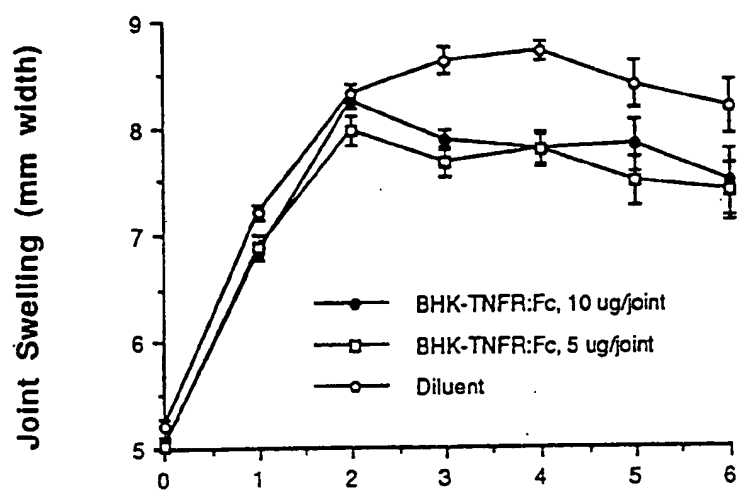


FIGURE 3

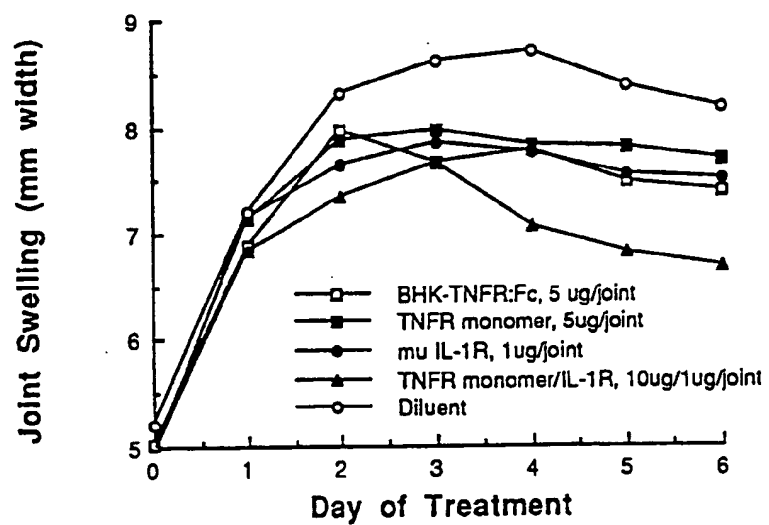


FIGURE 4

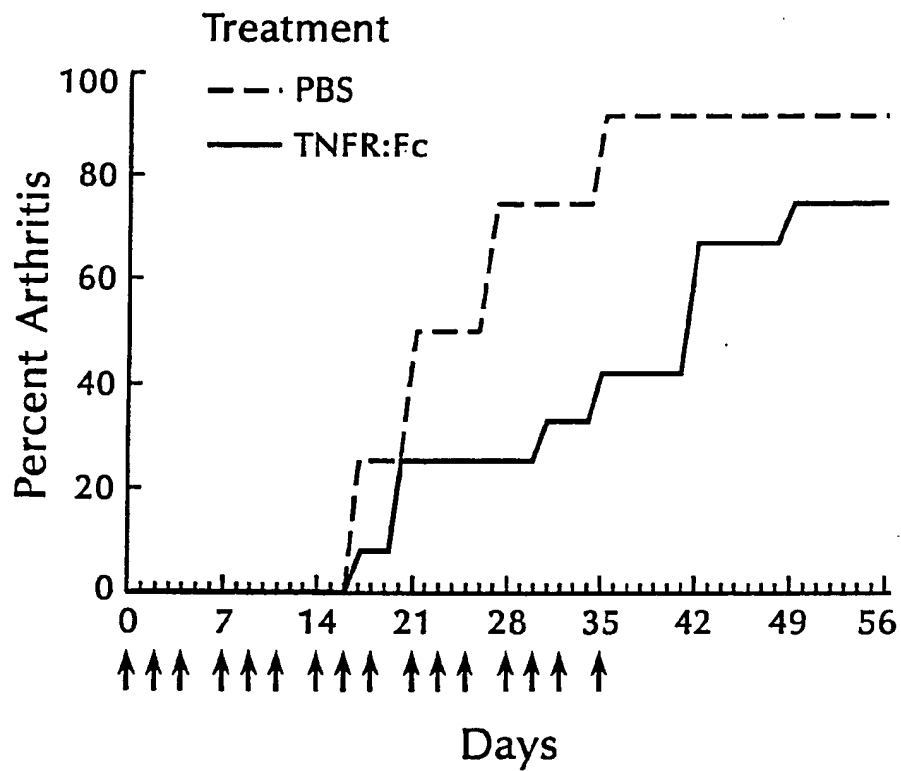


Figure 5

5 / 6

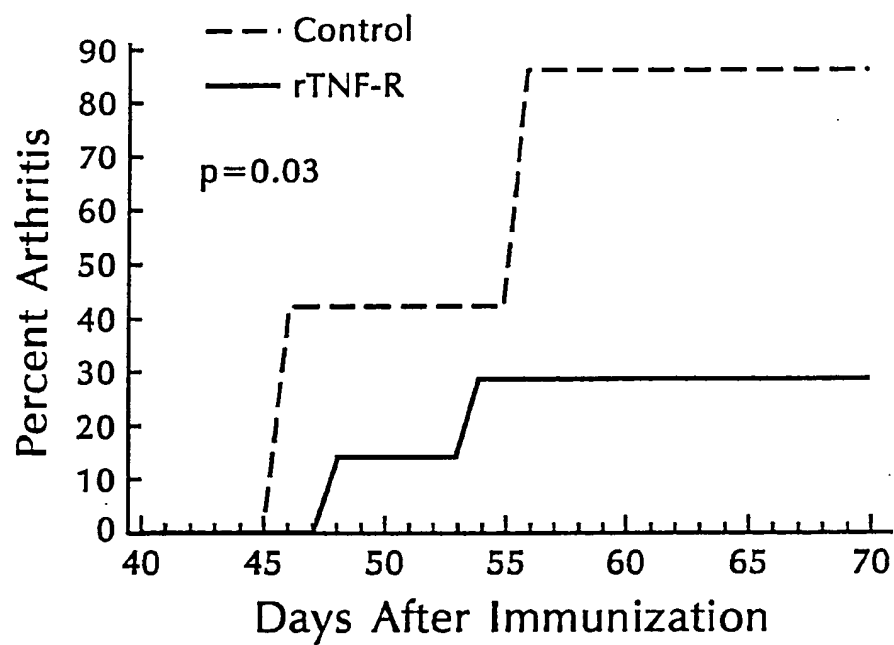


Figure 6

6 / 6

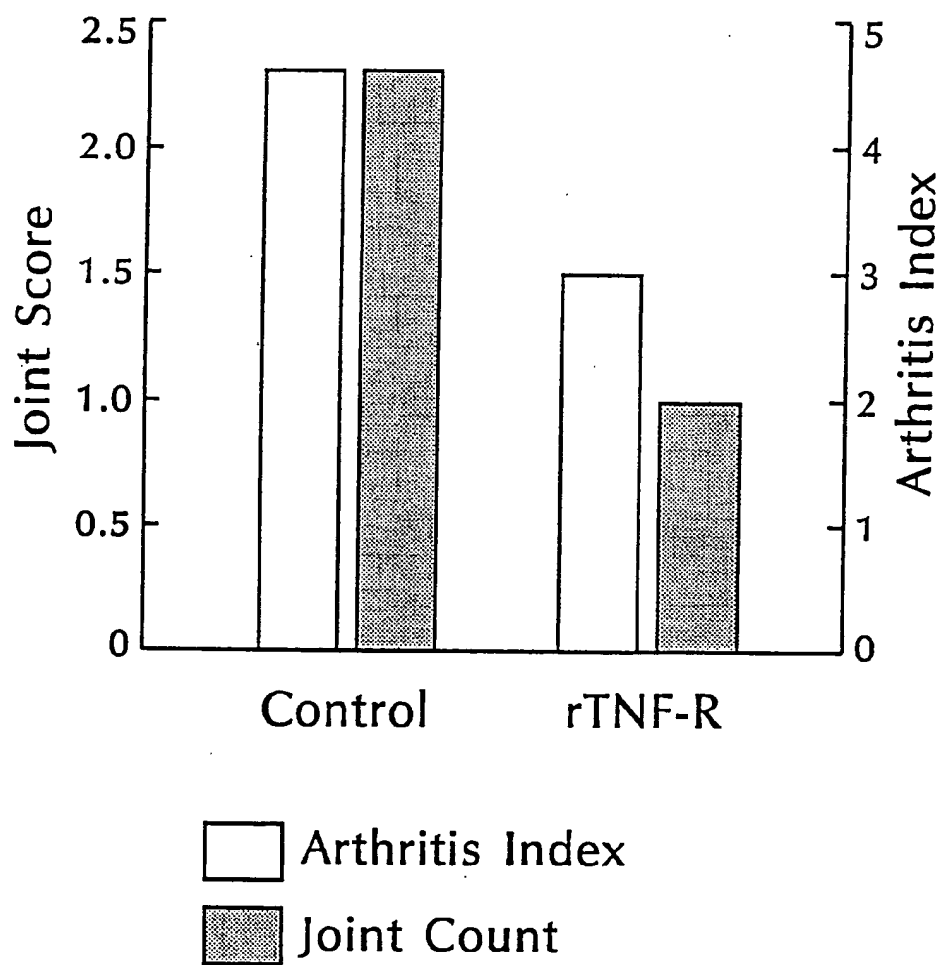


Figure 7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/08666

A. CLASSIFICATION OF SUBJECT MATTER IPC(5) : Please See Extra Sheet. US CL : Please See Extra Sheet. According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 424/85.1, 85.8; 935/15; 435/69.5, 69.7, 71.1, 172.1, 240.27, 972; 530/387.3, 391.7, 866 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	THE LANCET, ISSUED 29 JULY 1989, BRENNAN <i>ET AL.</i> , "INHIBITORY EFFECT OF TNF α ANTIBODIES ON SYNOVIAL CELL INTERLEUKIN-1 PRODUCTION IN RHEUMATOID ARTHRITIS", PAGES 244-247, SEE ENTIRE DOCUMENT. THE NEW ENGLAND JOURNAL OF MEDICINE, VOL. 322, No. 18, ISSUED 03 MAY 1990, HARRIS <i>ET AL.</i> , "MECHANISMS OF DISEASE: RHEUMATOID ARTHRITIS", PAGES 1277-1289, SEE ENTIRE DOCUMENT.	1-3
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Y		4-8, 8-9
Y		4-6, 8-9
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *A* document defining the general state of the art which is not considered to be part of particular relevance *E* earlier document published on or after the international filing date *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *O* document referring to an oral disclosure, use, exhibition or other means *P* document published prior to the international filing date but later than the priority date claimed *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *G* document member of the same patent family	
Date of the actual completion of the international search 01 DECEMBER 1993		Date of mailing of the international search report 28 DEC 1993
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. NOT APPLICABLE		Authorized officer T. MICHAEL NISBET <i>T. Nisbet for</i> Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US93/08666

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SCIENCE, VOL. 24, ISSUED 25 MAY 1990, SMITH <i>ET AL.</i> , "A RECEPTOR FOR TUMOR NECROSIS FACTOR DEFINES AN UNUSUAL FAMILY OF CELLULAR AND VIRAL PROTEINS", PAGES 1019-1023, SEE ENTIRE DOCUMENT.	4-6; 8-9
Y	US, A, 5,116,964 (CAPON <i>ET AL.</i>) 26 MAY 1992, SEE ENTIRE DOCUMENT.	6
Y	MOLECULAR IMMUNOLOGY, VOL. 28, No. 9, ISSUED 1991, HOOGENBOOM <i>ET AL.</i> , "CONSTRUCTION AND EXPRESSION OF ANTIBODY-TUMOR NECROSIS FACTOR FUSION PROTEINS", PAGES 1027-1037, SEE ENTIRE DOCUMENT.	6
A,P	JOURNAL OF CLINICAL INVESTIGATION, VOL. 91, ISSUED APRIL 1993, "THE POWER OF NEGATIVE THINKING", PAGES 1265-1266, SEE ENTIRE DOCUMENT.	1-9

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US93/08666

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (5):

A61K 45/05, 39/00, 35/14; C07K 3/00, 13/00, 15/00; C12P 21/06, 21/04; C12N 15/00, 5/00

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

424/85.1, 85.8; 935/15; 435/69.5, 69.7, 71.1, 172.1, 240.27, 972; 530/387.3, 391.7, 866